

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/567,536
Source: IFW
Date Processed by STIC: 1/5/07

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IFWO

RAW SEQUENCE LISTING

DATE: 01/05/2007

PATENT APPLICATION: US/10/567,536

TIME: 14:14:51

Input Set : N:\efs\01_05_07\10567536_efs\Seqlist.txt

Output Set: N:\CRF4\01052007\J567536.raw

4 <110> APPLICANT: HITCHMAN, Tim
 5 ROBERTSON, Dan E.
 6 HIRAIWA, Masao
 7 PHILLIPS, Yoko
 8 GRAY, Kevin
 10 <120> TITLE OF INVENTION: LACCASES, NUCLEIC ACIDS ENCODING THEM AND METHODS
 11 FOR MAKING AND USING THEM
 13 <130> FILE REFERENCE: 564462012600
 15 <140> CURRENT APPLICATION NUMBER: US 10/567,536
 C--> 16 <141> CURRENT FILING DATE: 2006-02-07
 18 <150> PRIOR APPLICATION NUMBER: PCT/US2004/025932
 19 <151> PRIOR FILING DATE: 2004-08-11
 21 <150> PRIOR APPLICATION NUMBER: US 60/494,472
 22 <151> PRIOR FILING DATE: 2003-08-11
 24 <160> NUMBER OF SEQ ID NOS: 26
 26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 1542
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Unknown
 33 <220> FEATURE:
 34 <223> OTHER INFORMATION: Obtained from an environmental sample
 36 <400> SEQUENCE: 1
 37 atgacacgtg aaaaatttgt ggatgctctc ccaatcccag atacactaaa gccggtacag 60
 38 cagtcaaaaag atagcacata ctacgaagta accatggagg aatgctacca tcagcttcac 120
 39 cgcgatctcc ctccaacccg cttgtggggc tataacggtt tattccccgg tcccaccatt 180
 40 aaggccaaaa gaaatgaaaa cgtttatgtg aaatggatga ataaccttcc ttcagagcat 240
 41 tttcttccga ttgatcacac cattcatcac agtgacagcc agcatgccga acccgaggtg 300
 42 aaaaccgtcg ttcatttaca cggcggcgctc actccagatg acagcgacgg ttatcctgag 360
 43 gcctgggtttt ctaaagactt tgaacaaaca ggcccttatt ttaaacgaga ggtttaccat 420
 44 tatccaaatc agcagcgcg agctatttta tggatcacg atcatgctat ggcgctcacg 480
 45 aggctgaatg tgtatgccgg gctcatcggt gcttatatca tccatgaacc aaaggaaaaa 540
 46 cgctgaagc tcccatcagg tgaatacgat gtgccgcttt tgatcacgga ccgtacgatt 600
 47 aatgaagatg gctctttatt ttatccgagc ggaccggaaa acccttcacc gtcactgcct 660
 48 aatccgtcaa tcgttccagc cttttgcgga gatacaattc tcgtcaacgg gaaggcatgg 720
 49 ccatacatgg aggtcgaacc gagaaaatac cgcttccgcg tcatcaatgc ctctaatacg 780
 50 agaacatata acctgtcact tgataatggg ggagaattta tccagatcgg ttctgacggc 840
 51 ggacttttgc cgcgctccgt caagctaaac tctttcagta tcgcgccagc tgagcgcttt 900
 52 gatatcctca ttgacttcgc cgcgtttgaa ggacaatcga ttatttttagc aaacagcgag 960
 53 ggctgcggcg gcgacgttaa tccggaatac gacgcaaaca tcatgcaatt cagagtcaca 1020
 54 aaaccgttag ccaaaaaaga cgaaagcaga aagccaaaat acctggcatc ttacccttca 1080
 55 gtacggcacg aaagaataca aaacctccga acattgaagc tggcaggaac tcaagatcaa 1140
 56 tacggcagac ccgttcttct tcttaacaac aaacgctggc acgatcctgt cactgaagca 1200

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57 ccgaaagccg gttctaccga aatatggtcg atcatcaatc cgacacgcgg aacacatccc 1260
58 atccatcttc atttggcttc cttccgtgta ttggaccggc gccatttga tacagcccgt 1320
59 tttgaagagc gcggagaact ggcctacacc ggacccgccg ttccgccgcc accaagtga 1380
60 aaaggctgga aagacacggt tcagtccac gccggtgaag tcctgagaat cgccgtaaca 1440
61 ttcgggccat acactgggcg gtacgtatgg cattgccaca ttcttgagca tgaagactat 1500
62 gacatgatga gaccgatgga tgtgattgac cccataaat ca 1542
64 <210> SEQ ID NO: 2
65 <211> LENGTH: 514
66 <212> TYPE: PRT
67 <213> ORGANISM: Unknown
69 <220> FEATURE:
70 <223> OTHER INFORMATION: Obtained from an environmental sample
72 <400> SEQUENCE: 2
73 Met Thr Arg Glu Lys Phe Val Asp Ala Leu Pro Ile Pro Asp Thr Leu
74 1 5 10 15
75 Lys Pro Val Gln Gln Ser Lys Asp Ser Thr Tyr Tyr Glu Val Thr Met
76 20 25 30
77 Glu Glu Cys Tyr His Gln Leu His Arg Asp Leu Pro Pro Thr Arg Leu
78 35 40 45
79 Trp Gly Tyr Asn Gly Leu Phe Pro Gly Pro Thr Ile Lys Ala Lys Arg
80 50 55 60
81 Asn Glu Asn Val Tyr Val Lys Trp Met Asn Asn Leu Pro Ser Glu His
82 65 70 75 80
83 Phe Leu Pro Ile Asp His Thr Ile His His Ser Asp Ser Gln His Ala
84 85 90 95
85 Glu Pro Glu Val Lys Thr Val Val His Leu His Gly Gly Val Thr Pro
86 100 105 110
87 Asp Asp Ser Asp Gly Tyr Pro Glu Ala Trp Phe Ser Lys Asp Phe Glu
88 115 120 125
89 Gln Thr Gly Pro Tyr Phe Lys Arg Glu Val Tyr His Tyr Pro Asn Gln
90 130 135 140
91 Gln Arg Gly Ala Ile Leu Trp Tyr His Asp His Ala Met Ala Leu Thr
92 145 150 155 160
93 Arg Leu Asn Val Tyr Ala Gly Leu Ile Gly Ala Tyr Ile Ile His Glu
94 165 170 175
95 Pro Lys Glu Lys Arg Leu Lys Leu Pro Ser Gly Glu Tyr Asp Val Pro
96 180 185 190
97 Leu Leu Ile Thr Asp Arg Thr Ile Asn Glu Asp Gly Ser Leu Phe Tyr
98 195 200 205
99 Pro Ser Gly Pro Glu Asn Pro Ser Pro Ser Leu Pro Asn Pro Ser Ile
100 210 215 220
101 Val Pro Ala Phe Cys Gly Asp Thr Ile Leu Val Asn Gly Lys Ala Trp
102 225 230 235 240
103 Pro Tyr Met Glu Val Glu Pro Arg Lys Tyr Arg Phe Arg Val Ile Asn
104 245 250 255
105 Ala Ser Asn Thr Arg Thr Tyr Asn Leu Ser Leu Asp Asn Gly Gly Glu
106 260 265 270
107 Phe Ile Gln Ile Gly Ser Asp Gly Gly Leu Leu Pro Arg Ser Val Lys
108 275 280 285

```

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109 Leu Asn Ser Phe Ser Ile Ala Pro Ala Glu Arg Phe Asp Ile Leu Ile
110      290                      295                      300
111 Asp Phe Ala Ala Phe Glu Gly Gln Ser Ile Ile Leu Ala Asn Ser Glu
112 305                      310                      315                      320
113 Gly Cys Gly Gly Asp Val Asn Pro Glu Thr Asp Ala Asn Ile Met Gln
114                      325                      330                      335
115 Phe Arg Val Thr Lys Pro Leu Ala Gln Lys Asp Glu Ser Arg Lys Pro
116                      340                      345                      350
117 Lys Tyr Leu Ala Ser Tyr Pro Ser Val Arg His Glu Arg Ile Gln Asn
118                      355                      360                      365
119 Leu Arg Thr Leu Lys Leu Ala Gly Thr Gln Asp Gln Tyr Gly Arg Pro
120      370                      375                      380
121 Val Leu Leu Leu Asn Asn Lys Arg Trp His Asp Pro Val Thr Glu Ala
122 385                      390                      395                      400
123 Pro Lys Ala Gly Ser Thr Glu Ile Trp Ser Ile Ile Asn Pro Thr Arg
124                      405                      410                      415
125 Gly Thr His Pro Ile His Leu His Leu Val Ser Phe Arg Val Leu Asp
126                      420                      425                      430
127 Arg Arg Pro Phe Asp Thr Ala Arg Phe Glu Glu Arg Gly Glu Leu Ala
128                      435                      440                      445
129 Tyr Thr Gly Pro Ala Val Pro Pro Pro Pro Ser Glu Lys Gly Trp Lys
130      450                      455                      460
131 Asp Thr Val Gln Ser His Ala Gly Glu Val Leu Arg Ile Ala Val Thr
132 465                      470                      475                      480
133 Phe Gly Pro Tyr Thr Gly Arg Tyr Val Trp His Cys His Ile Leu Glu
134                      485                      490                      495
135 His Glu Asp Tyr Asp Met Met Arg Pro Met Asp Val Ile Asp Pro His
136                      500                      505                      510

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137 Lys Ser

140 <210> SEQ ID NO: 3

141 <211> LENGTH: 1626

142 <212> TYPE: DNA

143 <213> ORGANISM: Unknown

145 <220> FEATURE:

146 <223> OTHER INFORMATION: Obtained from an environmental sample

148 <400> SEQUENCE: 3

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149 atgttacgac cggaggatgc aacgcggcgt gcctttttgc acgcggccac tatgtcctgt      60
150 cttgtcgcgg ctggtgcgtc cggctcttctg acgctgcgcg aggtccgggc gcaaccccgt      120
151 gctgcgaatc cgcagttcat cccggacctc gagatccagt tgaacgctcg ggaagatcat      180
152 gtgtcgatcc tgccctggacc actcactcgc gtctggcggt acgacggcaa agtcgtgaag      240
153 ggcgatccgg gcaacctggc tttcctgtcg aacggttatt taccctgggt gcgcgtgcgg      300
154 cgcgacagaa aagtgcgcat cgatttcgtc aaccagttag ctgagccgac catcatccac      360
155 tggcatggcc tgtacgtgcc agcagcaatg gatggacatc cgcgcaatgc ggttttcgacc      420
156 ggcgagcaact acgtgtacga gttcgagatc gcccaaccagg cagggaacgta ctggtttcat      480
157 gcgcaccccg acggtcgtac gggagcacia atttacttcg gactggcggg ggtattgatc      540
158 gtcgacgatg aggaggcggc cgccgggttg cccgaaggtc cgtacgatgt accgctcgtg      600
159 attcaggacc gcacgttcga cgatcggaac cagttcacgt atctcgccga aggcaatgag      660
160 ggggatgatg gcggcatgat gggcaacggc ggcgatgatg gacgcggggg catgatgggc      720
161 ggaggcggca tggggcagat gatggcgcgg atgatgggtt tcctcgccga ccggattctc      780

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162 gtcaacggca agcccgactt cgtgctgccg gtggctgccc gtgcctatcg ccttcgtttg      840
163 ctgaatgggt cgaacacgcg tatctacaag cttgcgtgga gcgaccggac acccctcacg      900
164 gtaatcggtg cggacggcgg actgctggaa cggccggtga cgcgccaata cgtcacgctg      960
165 gcgccggccg agcgcgtgga cgtctgggtg gatttcagtc gatggccggt cggcacgaag     1020
166 ctgacgctgc agagtctggc gttcgacggc gtccctggcca tgggcggcat gatcggcaac     1080
167 acctcggtac cgagcggcgc gtcgttcccc gtccctgaagg tcggcgtcga ccagcgtgcg     1140
168 aacacaaaaga tggaaactgcc ggcgcggctc gcacgcgtgc caccggtgcg ccctcaggac     1200
169 gccgtcaatg cgcacaatcc gaagggtgtt aacatcacga tgggcatgat ggtctggggc     1260
170 gtcaacgggc gtcgcttcga aatgaacggg gtggcgaaaa cgagaccgtg gagacgcaac     1320
171 agcacggaaa tctgggagtt ccgcaacgag gaatcgatga tgctgatggc ccattcgatg     1380
172 cacgttcacg ggctgcagtt ccgtgtgctg gagcgtaccg tccagccgga tttcagagcc     1440
173 ggttaccgca cgctggcagc gggactgggt gatgatggct ggaaagacac cgtgctattg     1500
174 atgcccggtg agcgtatccg cctgctgctc cggttcgca gctacacggg cctgtttctt     1560
175 taccattgtc acatgctgga gcacgaagat tccggattga tgcgtaacta cctgatccag     1620
176 acgtaa                                           1626

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178 <210> SEQ ID NO: 4

179 <211> LENGTH: 541

180 <212> TYPE: PRT

181 <213> ORGANISM: Unknown

183 <220> FEATURE:

184 <223> OTHER INFORMATION: Obtained from an environmental sample

186 <220> FEATURE:

187 <221> NAME/KEY: SIGNAL

188 <222> LOCATION: (1)...(37)

190 <400> SEQUENCE: 4

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191 Met Leu Arg Pro Glu Asp Ala Thr Arg Arg Ala Phe Leu His Ala Ala
192   1           5           10           15
193 Thr Met Ser Cys Leu Val Ala Ala Gly Ala Ser Gly Leu Leu Thr Leu
194           20           25           30
195 Arg Glu Val Arg Ala Gln Pro Arg Ala Ala Asn Pro Gln Phe Ile Pro
196           35           40           45
197 Asp Leu Glu Ile Gln Leu Asn Ala Arg Glu Asp His Val Ser Ile Leu
198           50           55           60
199 Pro Gly Pro Leu Thr Arg Val Trp Arg Tyr Asp Gly Lys Val Val Lys
200  65           70           75           80
201 Gly Asp Pro Gly Asn Leu Ala Phe Leu Ser Asn Gly Tyr Leu Pro Val
202           85           90           95
203 Val Arg Val Arg Arg Gly Gln Lys Val Arg Ile Asp Phe Val Asn Gln
204           100          105          110
205 Leu Ala Glu Pro Thr Ile Ile His Trp His Gly Leu Tyr Val Pro Ala
206           115          120          125
207 Ala Met Asp Gly His Pro Arg Asn Ala Val Ser Thr Gly Glu His Tyr
208           130          135          140
209 Val Tyr Glu Phe Glu Ile Ala Asn Gln Ala Gly Thr Tyr Trp Phe His
210 145          150          155          160
211 Ala His Pro Asp Gly Arg Thr Gly Ala Gln Ile Tyr Phe Gly Leu Ala
212           165          170          175
213 Gly Val Leu Ile Val Asp Asp Glu Glu Ala Ala Ala Gly Leu Pro Glu
214           180          185          190

```

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215 Gly Pro Tyr Asp Val Pro Leu Val Ile Gln Asp Arg Thr Phe Asp Asp
216      195      200      205
217 Arg Asn Gln Phe Thr Tyr Leu Ala Glu Gly Asn Glu Gly Met Met Gly
218      210      215      220
219 Gly Met Met Gly Asn Gly Gly Met Met Gly Arg Gly Gly Met Met Gly
220 225      230      235      240
221 Gly Gly Gly Met Gly Gln Met Met Ala Arg Met Met Gly Phe Leu Gly
222      245      250      255
223 Asp Arg Ile Leu Val Asn Gly Lys Pro Asp Phe Val Leu Pro Val Ala
224      260      265      270
225 Ala Arg Ala Tyr Arg Leu Arg Leu Leu Asn Gly Ser Asn Thr Arg Ile
226      275      280      285
227 Tyr Lys Leu Ala Trp Ser Asp Arg Thr Pro Leu Thr Val Ile Gly Thr
228      290      295      300
229 Asp Gly Gly Leu Leu Glu Arg Pro Val Thr Arg Gln Tyr Val Thr Leu
230 305      310      315      320
231 Ala Pro Ala Glu Arg Val Asp Val Trp Val Asp Phe Ser Arg Trp Pro
232      325      330      335
233 Val Gly Thr Lys Leu Thr Leu Gln Ser Leu Ala Phe Asp Gly Val Leu
234      340      345      350
235 Ala Met Gly Gly Met Ile Gly Asn Thr Ser Leu Pro Ser Gly Ala Ser
236      355      360      365
237 Phe Pro Val Leu Lys Val Gly Val Asp Gln Arg Ala Asn Thr Lys Met
238      370      375      380
239 Glu Leu Pro Ala Arg Leu Ala Ser Leu Pro Pro Val Arg Pro Gln Asp
240 385      390      395      400
241 Ala Val Asn Ala His Asn Pro Lys Val Phe Asn Ile Thr Met Gly Met
242      405      410      415
243 Met Val Trp Gly Val Asn Gly Arg Arg Phe Glu Met Asn Gly Val Ala
244      420      425      430
245 Lys Thr Glu Thr Val Arg Arg Asn Ser Thr Glu Ile Trp Glu Phe Arg
246      435      440      445
247 Asn Glu Glu Ser Met Met Leu Met Ala His Ser Met His Val His Gly
248      450      455      460
249 Leu Gln Phe Arg Val Leu Glu Arg Thr Val Gln Pro Asp Phe Arg Ala
250 465      470      475      480
251 Gly Tyr Arg Thr Leu Ala Ala Gly Leu Val Asp Asp Gly Trp Lys Asp
252      485      490      495
253 Thr Val Leu Leu Met Pro Gly Glu Arg Ile Arg Leu Leu Leu Arg Phe
254      500      505      510
255 Ala Ser Tyr Thr Gly Leu Phe Leu Tyr His Cys His Met Leu Glu His
256      515      520      525
257 Glu Asp Ser Gly Leu Met Arg Asn Tyr Leu Ile Gln Thr
258      530      535      540
260 <210> SEQ ID NO: 5
261 <211> LENGTH: 1584
262 <212> TYPE: DNA
263 <213> ORGANISM: Bacteria
265 <400> SEQUENCE: 5

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VERIFICATION SUMMARY

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Input Set : N:\efs\01_05_07\10567536_efs\Seqlist.txt

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date